

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2005, 11:04:38 ; Search time 160 Seconds
(without alignments)
633.880 Million cell updates/sec

Title: US-09-826-212A-2

Perfect score: 1382
Sequence: 1 MARPKTLKRVVIVAVILP.....YLCTGIYIVLIVLIVFV 259

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications AA:
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2: /cgn2_6/ptodata/2/pubpaa/PCTI_NEM_PUB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	1382	100.0	259	9	US-09-887-879-1	Sequence 1, Appli
3	1382	100.0	259	9	US-09-992-964-1	Sequence 300, App
4	1382	100.0	259	14	US-10-028-072-300	Sequence 300, App
5	1382	100.0	259	14	US-10-140-808-300	Sequence 300, App
6	1382	100.0	259	14	US-10-121-049-300	Sequence 300, App
7	1382	100.0	259	14	US-10-133-904-300	Sequence 300, App
8	1382	100.0	259	14	US-10-140-470-300	Sequence 300, App
9	1382	100.0	259	14	US-10-175-746-300	Sequence 300, App
10	1382	100.0	259	14	US-10-176-918-300	Sequence 300, App
11	1382	100.0	259	14	US-10-176-921-300	Sequence 300, App

12	1382	100.0	259	14	US-10-137-865-300	Sequence 300, App
13	1382	100.0	259	14	US-10-140-474-300	Sequence 300, App
14	1382	100.0	259	14	US-10-142-431-300	Sequence 300, App
15	1382	100.0	259	14	US-10-143-114-300	Sequence 300, App
16	1382	100.0	259	14	US-10-142-419-300	Sequence 300, App
17	1382	100.0	259	14	US-10-123-262-300	Sequence 300, App
18	1382	100.0	259	14	US-10-142-423-300	Sequence 300, App
19	1382	100.0	259	14	US-10-121-050-300	Sequence 300, App
20	1382	100.0	259	14	US-10-141-755-300	Sequence 300, App
21	1382	100.0	259	14	US-10-143-032-300	Sequence 300, App
22	1382	100.0	259	14	US-10-123-108-300	Sequence 300, App
23	1382	100.0	259	14	US-10-123-236-300	Sequence 300, App
24	1382	100.0	259	14	US-10-123-261-300	Sequence 300, App
25	1382	100.0	259	14	US-10-140-921-300	Sequence 300, App
26	1382	100.0	259	14	US-10-140-928-300	Sequence 300, App
27	1382	100.0	259	14	US-10-121-045-300	Sequence 300, App
28	1382	100.0	259	14	US-10-123-292-300	Sequence 300, App
29	1382	100.0	259	14	US-10-123-903-300	Sequence 300, App
30	1382	100.0	259	14	US-10-124-819-300	Sequence 300, App
31	1382	100.0	259	14	US-10-124-822-300	Sequence 300, App
32	1382	100.0	259	14	US-10-140-925-300	Sequence 300, App
33	1382	100.0	259	14	US-10-160-498-300	Sequence 300, App
34	1382	100.0	259	14	US-10-124-824-300	Sequence 300, App
35	1382	100.0	259	14	US-10-127-825A-300	Sequence 300, App
36	1382	100.0	259	14	US-10-127-829A-300	Sequence 300, App
37	1382	100.0	259	14	US-10-127-835A-300	Sequence 300, App
38	1382	100.0	259	14	US-10-127-839A-300	Sequence 300, App
39	1382	100.0	259	14	US-10-127-901A-300	Sequence 300, App
40	1382	100.0	259	14	US-10-128-693A-300	Sequence 300, App
41	1382	100.0	259	14	US-10-131-813A-300	Sequence 300, App
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43	1382	100.0	259	14	US-10-131-823A-300	Sequence 300, App
44	1382	100.0	259	14	US-10-131-824A-300	Sequence 300, App
45	1382	100.0	259	14	US-10-131-830A-300	Sequence 300, App

ALIGNMENTS

RESULT 1
US-09-826-212-2
Sequence 2, Application US/09826212
Patent No. US2001002156A1
GENERAL INFORMATION:
APPLICANT: Wei, Yang-Pei
APPLICANT: Gentz, Reiner
APPLICANT: Ruben, Steven
APPLICANT: Ni, Jian
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488, 128006
CURRENT APPLICATION NUMBER: US/09/826, 212
CURRENT FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 259
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-212-2

Query Match 100.0%; Score 1382; DB 9; Length 259;
Best Local Similarity 100.0%; Pred. No. 2, 1e-85;
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPKTLKRVVIVAVILPVLAYSATTAQREYPOOTVAPOOQRHSFKRECPAGSHRS 60
DB 1 MARPKTLKRVVIVAVILPVLAYSATTAQREYPOOTVAPOOQRHSFKRECPAGSHRS 60
QY 61 EHTACNCPCEGVVYTNANNNRSCPCCTVCKSDOKHSCTMTRDVYCOCKEGTFNEN 120
DB 61 EHTACNCPCEGVVYTNANNNRSCPCCTVCKSDOKHSCTMTRDVYCOCKEGTFNEN 120
QY 121 SPENCRCRSCPSGSEVSNCTSDMDIQCVBEFGANATVETPAABETMTNTSPGPAPAAE 180

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OM protein - protein search, using BW model

Run on: August 17, 2005, 10:58:37 ; Search time 23 Seconds
(Without alignments)
840.613 Million cell updates/sec

Title: US-09-826-212a-2

Perfect score: 1382
Sequence: 1 MARIPKLVVVVAVLVLP.....YLSTRIIVLIVLVV 259

Scoring table: BLOSUM62
Gapop: 10.0, Gapext: 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

- Issued Patents AA:*
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 - 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
 - 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
 - 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
 - 5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
 - 6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1382	100.0	299	4	US-09-114-618-4
5	1382	100.0	299	4	US-09-949-016-6422
6	1376	99.6	301	4	US-09-949-016-9189
7	634	45.9	386	3	US-09-086-483A-2
8	634	45.9	386	4	US-09-580-212-2
9	634	45.9	386	4	US-09-769-402-2
10	627	45.4	386	4	US-09-130-491-6
11	480	34.7	452	4	US-09-949-016-9855
12	472	34.2	234	4	US-09-130-491-12
13	472	34.2	467	4	US-09-086-483A-6
14	472	34.2	467	4	US-09-580-212-6
15	472	34.2	467	4	US-09-565-918-2
16	472	34.2	467	3	US-09-013-895A-2
17	472	34.2	468	4	US-09-448-868-2
18	472	34.2	468	4	US-09-949-016-6423
19	452	32.7	350	4	US-09-134-618-6
20	448	32.4	440	4	US-09-536-201-2
21	448	32.4	440	4	US-09-578-192-2
22	448	32.4	440	4	US-09-578-192-2
23	398.5	28.8	444	3	US-09-333-593A-8
24	383.5	27.7	411	3	US-09-134-618-2
25	380.5	27.5	412	3	US-09-333-593A-2
26	379.5	27.5	411	3	US-09-329-633A-2

28	379.5	27.5	411	3	US-09-079-029-1	Sequence 1, Appl1
29	379.5	27.5	411	3	US-09-874-138-2	Sequence 2, Appl1
30	366.5	17.1	303	3	US-09-333-593A-4	Sequence 4, Appl1
31	212	15.3	368	2	US-08-651-579-2	Sequence 2, Appl1
32	201.5	14.6	427	3	US-09-086-483A-4	Sequence 4, Appl1
33	201.5	14.6	427	3	US-09-041-886-2	Sequence 2, Appl1
34	201.5	14.6	427	3	US-09-006-353A-5	Sequence 5, Appl1
35	201.5	14.6	427	4	US-09-573-986-5	Sequence 5, Appl1
36	201.5	14.6	427	4	US-09-769-402-4	Sequence 4, Appl1
37	201.5	14.6	427	4	US-09-580-212-4	Sequence 4, Appl1
38	201.5	14.6	427	4	US-09-748-537-13	Sequence 13, Appl1
39	201.5	14.6	427	4	US-09-949-016-6233	Sequence 24, Appl1
40	201.5	14.6	427	4	US-09-527-236A-4	Sequence 6233, Ap
41	201.5	14.6	455	3	US-09-756-854-4	Sequence 4, Appl1
42	201.5	14.6	464	4	US-09-949-016-9441	Sequence 9441, Ap
43	201.5	14.5	425	4	US-09-748-537-14	Sequence 14, Appl1
44	200.5	14.5	425	4	US-09-612-033B-14	Sequence 14, Appl1
45	198	14.3	398	4	US-09-612-033B-14	Sequence 14, Appl1

ALIGNMENTS

RESULT 1
US-09-006-353A-2
Sequence 2, Application US/09006353A
Patent No. 6261801

GENERAL INFORMATION:

APPLICANT: WEI, YING-PEI

APPLICANT: YU, GUO-LIANG

APPLICANT: GENTZ, REINER

APPLICANT: RUBEN, STEVEN

TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/006,353A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BROOKS, ANDERS A

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF311

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 259 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: protein

US-09-006-353A-2

Query Match 100.0%; Score 1382; DB 3; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.4e-101;
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MARIPKLVVVVAVLVLPVLAISATTAARQREVPQQTVAPOQQRHSFKGBECPPAGSHS 60
1 MARIPKLVVVVAVLVLPVLAISATTAARQREVPQQTVAPOQQRHSFKGBECPPAGSHS 60

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OM nucleic - nucleic search, using BW model

Run on: August 19, 2005, 06:54:16 ; Search time 988 Seconds
(without alignments)
9153.554 Million cell updates/sec

Title: US-09-826-212A-1
Perfect score: 1392
Sequence: 1 cctctccacgcgcagcaact.....agatttcctcgtaaaaaaa 1392

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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4	1103	79.2	1180	9	US-09-887-879-2
5	1103	79.2	1180	9	US-09-887-879-4
6	1103	79.2	1180	9	US-09-992-964-2
7	1103	79.2	1180	9	US-09-992-964-4

8	1103	79.2	1180	15	US-10-242-383-2	Sequence 2, Appl1
9	1103	79.2	1180	15	US-10-242-383-4	Sequence 4, Appl1
10	1092	78.4	1102	14	US-10-028-072-299	Sequence 299, App
11	1092	78.4	1102	14	US-10-140-868-299	Sequence 299, App
12	1092	78.4	1102	14	US-10-121-049-299	Sequence 299, App
13	1092	78.4	1102	14	US-10-123-904-299	Sequence 299, App
14	1092	78.4	1102	14	US-10-140-470-299	Sequence 299, App
15	1092	78.4	1102	14	US-10-175-746-299	Sequence 299, App
16	1092	78.4	1102	14	US-10-175-918-299	Sequence 299, App
17	1092	78.4	1102	14	US-10-137-865-299	Sequence 299, App
18	1092	78.4	1102	14	US-10-140-474-299	Sequence 299, App
19	1092	78.4	1102	14	US-10-142-431-299	Sequence 299, App
20	1092	78.4	1102	14	US-10-143-114-299	Sequence 299, App
21	1092	78.4	1102	14	US-10-142-423-299	Sequence 299, App
22	1092	78.4	1102	14	US-10-123-262-299	Sequence 299, App
23	1092	78.4	1102	14	US-10-123-262-299	Sequence 299, App
24	1092	78.4	1102	14	US-10-121-050-299	Sequence 299, App
25	1092	78.4	1102	14	US-10-141-755-299	Sequence 299, App
26	1092	78.4	1102	14	US-10-143-032-299	Sequence 299, App
27	1092	78.4	1102	14	US-10-123-108-299	Sequence 299, App
28	1092	78.4	1102	14	US-10-123-236-299	Sequence 299, App
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41	1092	78.4	1102	14	US-10-127-825A-299	Sequence 299, App
42	1092	78.4	1102	14	US-10-127-825A-299	Sequence 299, App
43	1092	78.4	1102	14	US-10-127-825A-299	Sequence 299, App
44	1092	78.4	1102	14	US-10-127-825A-299	Sequence 299, App
45	1092	78.4	1102	14	US-10-127-825A-299	Sequence 299, App

ALIGNMENTS

RESULT 1
US-09-826-212-1
Sequence 1, Application US/09826212
Patent No. US20010021516A1
GENERAL INFORMATION:
APPLICANT: Wei, Ying-Fel
APPLICANT: Gentz, Reiner
APPLICANT: Ruben, Steven
APPLICANT: Ni, Jian
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.128006
CURRENT APPLICATION NUMBER: US/09/826.212
CURRENT FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 1392
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (183)..(959)
NAME/KEY: mat.peptide
LOCATION: (261)..()
NAME/KEY: sig.peptide
LOCATION: (183)..(260)
US-09-826-212-1
Query Match: 100.0%; Score 1392; DB 9; Length 1392;
Best Local Similarity: 100.0%; Pred. No. 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model.

Run on: August 19, 2005, 04:06:21 ; Search time 264 Seconds
(without alignments)
8627.641 Million cell updates/sec

Title: US-09-826-212a-1

Perfect score: 1392
Sequence: 1 cctctccagcgacgacgaact.....agatttcggtgaaaaaaa 1392

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

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3: /cgn2_6/prodata/1/ina/5B COMB.seq:
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6: /cgn2_6/prodata/1/ina/Backfillseq.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1392	100.0	3	US-09-006-353A-1
2	1392	100.0	3	US-09-573-986-1
3	1311.6	94.2	4	US-09-949-016-551
4	1310.8	94.2	4	US-09-949-016-3318
5	898.4	64.5	3	US-09-134-618-3
6	801.8	57.6	4	US-09-949-016-15060
7	801.8	57.6	4	US-09-949-016-12293
8	598	43.0	601	US-09-949-016-119469
9	598	43.0	601	US-09-949-016-119469
10	561.4	40.3	601	US-09-949-016-119469
11	561.4	40.3	601	US-09-949-016-119469
12	473	34.0	601	US-09-949-016-28872
13	473	34.0	601	US-09-949-016-119467
14	426.8	30.7	3566	US-09-886-483A-1
15	426.8	30.7	3566	US-09-886-483A-1
16	426.8	30.7	3566	US-09-886-483A-1
17	426.8	30.7	3566	US-09-886-483A-1
18	372.8	26.8	398	US-09-580-212-15
19	372.8	26.8	398	US-09-580-212-15
20	372.8	26.8	398	US-09-580-212-15
21	358.6	25.8	50186	US-09-949-016-14066
22	321.2	23.1	506	US-09-006-353A-15
23	321.2	23.1	506	US-09-573-986-15
24	300.6	21.6	66175	US-09-949-016-12293
25	256.2	18.4	1407	US-09-134-618-5
26	256.2	18.4	1407	US-09-505-250-2
27	256.2	18.4	4	US-09-949-016-552

28	256.2	18.4	2152	3	US-09-013-895A-1	Sequence 1, Appl1
29	256.2	18.4	2152	3	US-09-565-918-1	Sequence 1, Appl1
30	256.2	18.4	2152	3	US-09-448-868-1	Sequence 1, Appl1
31	256	18.4	1323	4	US-08-883-036A-1	Sequence 1, Appl1
32	256	18.4	1323	4	US-09-536-201-1	Sequence 1, Appl1
33	256	18.4	1323	4	US-09-578-392-1	Sequence 1, Appl1
34	247	17.7	1408	4	US-09-949-016-3984	Sequence 16, Appl1
35	244.2	17.5	325	3	US-09-006-353A-16	Sequence 16, Appl1
36	244.2	17.5	325	3	US-09-573-986-16	Sequence 16, Appl1
37	244	17.5	601	4	US-09-949-016-28838	Sequence 119433, A
38	244	17.5	601	4	US-09-949-016-119433	Sequence 119433, A
39	243.4	17.5	37622	4	US-09-949-016-12294	Sequence 15726, A
40	243.4	17.5	37622	4	US-09-949-016-15726	Sequence 15726, A
41	242.2	17.4	1799	3	US-09-329-633A-1	Sequence 1, Appl1
42	242.2	17.4	1799	3	US-09-079-029-2	Sequence 2, Appl1
43	240.8	17.3	1600	4	US-09-874-138-1	Sequence 1, Appl1
44	239.8	17.2	3881	3	US-09-333-593A-1	Sequence 1, Appl1
45	226.2	16.2	1236	3	US-09-134-618-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-006-353A-1
Sequence 1, Application US/09006353A
Patent No. 6261801
GENERAL INFORMATION:
APPLICANT: WEI, YING-FEI
APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKS, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF841
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURES:
NAME/KEY: CDS
LOCATION: 183..959
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 183..260
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 261..959